RAW SEQUENCE LISTING ERROR REPORT
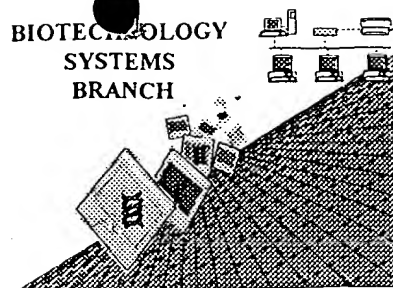
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

RECEIVED

JUN 0 4 2001

TECH CENTER 1600/2900

Application Serial Number: ___09/781, 712 A___

Source: ___1635___

Date Processed by STIC: ___5-17-01___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/781,712 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ✓ Use of "Artificial" (NEW RULES)
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

1635

RAW SEQUENCE LISTING   DATE: 05/17/2001
PATENT APPLICATION: US/09/781,712A   TIME: 10:13:22

Input Set : A:\es.txt
Output Set: N:\CRF3\05172001\I781712A.raw

```
 5 <110> APPLICANT: Crooke, Stanley T.
 6         Lima, Walter
.7         Wu, Hongjiang
 9 <120> TITLE OF INVENTION: Methods of Using Mammalian RNase H and Compositions Thereof
12 <130> FILE REFERENCE: ISPH-0520
14 <140> CURRENT APPLICATION NUMBER: US/09/781,712A
15 <141> CURRENT FILING DATE: 2001-02-12
17 <150> PRIOR APPLICATION NUMBER: US 09/684,254
18 <151> PRIOR FILING DATE: 2000-10-06
21 <150> PRIOR APPLICATION NUMBER: US 09/343,809
22 <151> PRIOR FILING DATE: 1999-06-30
25 <150> PRIOR APPLICATION NUMBER: US 09/203,716
26 <151> PRIOR FILING DATE: 1998-12-02
29 <150> PRIOR APPLICATION NUMBER: US 60/067,458
30 <151> PRIOR FILING DATE: 1997-12-04
33 <160> NUMBER OF SEQ ID NOS: 39
36 <170> SOFTWARE: PatentIn version 3.0
39 <210> SEQ ID NO: 1
41 <211> LENGTH: 299
43 <212> TYPE: PRT
45 <213> ORGANISM: Homo sapiens
49 <400> SEQUENCE: 1
51 Met Asp Leu Ser Glu Leu Glu Arg Asp Asn Thr Gly Arg Cys Arg Leu
52 1               5                   10                  15
54 Ser Ser Pro Val Pro Ala Val Cys Arg Lys Glu Pro Cys Val Leu Gly
55             20                  25                  30
57 Val Asp Glu Ala Gly Arg Gly Pro Val Leu Gly Pro Met Val Tyr Ala
58         35          .           40                  45
60 Ile Cys Tyr Cys Pro Leu Pro Arg Leu Ala Asp Leu Glu Ala Leu Lys
61     50                  55                  60
63 Val Ala Asp Ser Lys Thr Leu Leu Glu Ser Glu Arg Glu Arg Leu Phe
64 65                  70                  75                  80
66 Ala Lys Met Glu Asp Thr Asp Phe Val Gly Trp Ala Leu Asp Val Leu
67             85                  90                  95
69 Ser Pro Asn Leu Ile Ser Thr Ser Met Leu Gly Trp Val Lys Tyr Asn
70             100                 105                 110
72 Leu Asn Ser Leu Ser His Asp Thr Ala Thr Gly Leu Ile Gln Tyr Ala
73             115                 120                 125
75 Leu Asp Gln Gly Val Asn Val Thr Gln Val Phe Val Asp Thr Val Gly
76     130                 135                 140
78 Met Pro Glu Thr Tyr Gln Ala Arg Leu Gln Gln Ser Phe Pro Gly Ile
79 145                 150                 155                 160
81 Glu Val Thr Val Lys Ala Lys Ala Asp Ala Leu Tyr Pro Val Val Ser
82             165                 170                 175
84 Ala Ala Ser Ile Cys Ala Lys Val Ala Arg Asp Gln Ala Val Lys Lys
85             180                 185                 190
87 Trp Gln Phe Val Glu Lys Leu Gln Asp Leu Asp Thr Asp Tyr Gly Ser
```

```
 88            195                200                205
 90 Gly Tyr Pro Asn Asp Pro Lys Thr Lys Ala Trp Leu Lys Glu His Val
 91      210                215                220
 93 Glu Pro Val Phe Gly Phe Pro Gln Phe Val Arg Phe Ser Trp Arg Thr
 94 225                230                235                240
 96 Ala Gln Thr Ile Leu Glu Lys Glu Ala Glu Asp Val Ile Trp Glu Asp
 97               245                250                255
 99 Ser Ala Ser Glu Asn Gln Glu Gly Leu Arg Lys Ile Thr Ser Tyr Phe
100               260                265                270
102 Leu Asn Glu Gly Ser Gln Ala Arg Pro Arg Ser Ser His Arg Tyr Phe
103           275                280                285
105 Leu Glu Arg Gly Leu Glu Ser Ala Thr Ser Leu
106      290                295
108 <210> SEQ ID NO: 2
110 <211> LENGTH: 128
112 <212> TYPE: PRT
114 <213> ORGANISM: Mus sp.
118 <400> SEQUENCE: 2
120 Met Asp Leu Ser Glu Leu Glu Arg Asp Asn Thr Gly Arg Cys Arg Leu
121 1             5                10                15
123 Ser Ser Pro Val Pro Ala Val Cys Leu Lys Glu Pro Cys Val Leu Gly
125               20                25                30
127 Val Asp Glu Ala Gly Arg Gly Pro Val Leu Gly Pro Met Val Tyr Ala
128           35                40                45
130 Ile Cys Tyr Cys Pro Leu Ser Arg Leu Ala Asp Leu Glu Ala Leu Lys
131      50                55                60
133 Val Ala Asp Ser Lys Thr Leu Thr Glu Asn Glu Arg Glu Arg Leu Phe
134 65                70                75                 80
136 Ala Lys Met Glu Glu Asp Gly Asp Phe Val Gly Trp Ala Leu Asp Val
137               85                90                95
139 Leu Ser Pro Asn Leu Ile Ser Thr Ser Met Leu Gly Arg Val Lys Tyr
140               100               105               110
142 Asn Leu Asn Ser Leu Ser His Asp Thr Ala Ala Gly Leu Ile Gln Tyr
143           115                120                125
145 <210> SEQ ID NO: 3
147 <211> LENGTH: 307
149 <212> TYPE: PRT
151 <213> ORGANISM: Caenorhabditis elegans
155 <400> SEQUENCE: 3
157 Ser Lys Thr Val Lys Tyr Phe Ile Glu Arg Met Ser Leu Lys Cys Glu
158 1             5                10                15
160 Thr Glu Arg Ser Lys Thr Trp Asn Asn Phe Gly Asn Gly Ile Pro Cys
161           20                25                30
163 Val Leu Gly Ile Asp Glu Ala Gly Arg Gly Pro Val Leu Gly Pro Met
164      35                40                45
166 Val Tyr Ala Ala Ala Ile Ser Pro Leu Asp Gln Asn Val Glu Leu Lys
167      50                55                60
169 Asn Leu Gly Val Asp Asp Ser Lys Ala Leu Asn Glu Ala Lys Arg Glu
170 65                70                75                 80
```

```
172 Glu Ile Phe Asn Lys Met Asn Glu Asp Glu Asp Ile Gln Gln Ile Ile
173               85                  90                  95
175 Ala Tyr Ala Leu Arg Cys Leu Ser Pro Glu Leu Ile Ser Cys Ser Met
176              100                 105                 110
178 Leu Lys Arg Gln Lys Tyr Ser Leu Asn Glu Val Ser His Glu Ala Ala
179          115                 120                 125
181 Ile Thr Leu Ile Arg Asp Ala Leu Ala Cys Asn Val Asn Val Val Glu
182      130                 135                 140
184 Ile Lys Val Asp Thr Val Gly Pro Lys Ala Thr Tyr Gln Ala Lys Leu
185 145              150                 155                 160
187 Glu Lys Leu Phe Pro Gly Ile Ser Ile Cys Val Thr Glu Lys Ala Asp
188              165                 170                 175
190 Ser Leu Phe Pro Ile Val Ser Ala Ala Ser Ile Ala Ala Lys Val Thr
191              180                 185                 190
193 Arg Asp Ser Arg Leu Arg Asn Trp Gln Phe Arg Glu Lys Asn Ile Lys
194          195                 200                 205
196 Val Pro Asp Ala Gly Tyr Gly Ser Gly Tyr Pro Gly Asp Pro Asn Thr
197      210                 215                 220
199 Lys Lys Phe Leu Gln Leu Ser Val Glu Pro Val Phe Gly Phe Cys Ser
200 225              230                 235                 240
202 Leu Val Arg Ser Ser Trp Lys Thr Ala Ser Thr Ile Val Glu Lys Arg
203              245                 250                 255
205 Cys Val Pro Gly Ser Trp Glu Asp Asp Glu Glu Glu Gly Lys Ser Gln
206              260                 265                 270
208 Ser Lys Arg Met Thr Ser Trp Met Val Pro Lys Asn Glu Thr Glu Val
209          275                 280                 285
211 Val Pro Lys Arg Asn Met Glu Ile Asn Leu Thr Lys Ile Val Ser Thr
212      290                 295                 300
214 Leu Phe Leu
215 305
217 <210> SEQ ID NO: 4
219 <211> LENGTH: 307
221 <212> TYPE: PRT
223 <213> ORGANISM: Saccharomyces cerevisiae
227 <400> SEQUENCE: 4
229 Met Val Pro Pro Thr Val Glu Ala Ser Leu Glu Ser Pro Tyr Thr Lys
230 1             5                  10                  15
232 Ser Tyr Phe Ser Pro Val Pro Ser Ala Leu Leu Glu Gln Asn Asp Ser
233          20                  25                  30
235 Pro Ile Ile Met Gly Ile Asp Glu Ala Gly Arg Gly Pro Val Leu Gly
236           35                 40                  45
238 Pro Met Val Tyr Ala Val Ala Tyr Ser Thr Gln Lys Tyr Gln Asp Glu
239      50                  55                  60
241 Thr Ile Ile Pro Asn Tyr Glu Phe Asp Asp Ser Lys Lys Leu Thr Asp
242 65                  70                  75.                 80
244 Pro Ile Arg Arg Met Leu Phe Ser Lys Ile Tyr Gln Asp Asn Glu Glu
245              85                  90                  95
247 Leu Thr Gln Ile Gly Tyr Ala Thr Thr Cys Ile Thr Pro Leu Asp Ile
249          100                 105                 110
```

RAW SEQUENCE LISTING   DATE: 05/17/2001
PATENT APPLICATION: US/09/781,712A   TIME: 10:13:22

Input Set : A:\es.txt
Output Set: N:\CRF3\05172001\I781712A.raw

```
251 Ser Arg Gly Met Ser Lys Phe Pro Pro Thr Arg Asn Tyr Asn Leu Asn
252         115             120             125
254 Glu Gln Ala His Asp Val Thr Met Ala Leu Ile Asp Gly Val Ile Lys
255         130             135             140
257 Gln Asn Val Lys Leu Ser His Val Tyr Val Asp Thr Val Gly Pro Pro
258 145             150             155             160
260 Ala Ser Tyr Gln Lys Lys Leu Glu Gln Arg Phe Pro Gly Val Lys Phe
261             165             170             175
263 Thr Val Ala Lys Lys Ala Asp Ser Leu Tyr Cys Met Val Ser Val Ala
264         180             185             190
266 Ser Val Val Ala Lys Val Thr Arg Asp Ile Leu Val Glu Ser Leu Lys
267         195             200             205
269 Arg Asp Pro Asp Glu Ile Leu Gly Ser Gly Tyr Pro Ser Asp Pro Lys
270         210             215             220
272 Thr Val Ala Trp Leu Lys Arg Asn Gln Thr Ser Leu Met Gly Trp Pro
273 225             230             235             240
275 Ala Asn Met Val Arg Phe Ser Trp Gln Thr Cys Gln Thr Leu Leu Asp
276             245             250             255
278 Asp Ala Ser Lys Asn Ser Ile Pro Ile Lys Trp Glu Glu Gln Tyr Met
279             260             265             270
281 Asp Ser Arg Lys Asn Ala Ala Gln Lys Thr Lys Gln Leu Gln Leu Gln
282         275             280             285
284 Met Val Ala Lys Pro Val Arg Arg Lys Arg Leu Arg Thr Leu Asp Asn
285         290             295             300
287 Trp Tyr Arg
288 305
290 <210> SEQ ID NO: 5
292 <211> LENGTH: 198
294 <212> TYPE: PRT
296 <213> ORGANISM: Escherichia coli
300 <400> SEQUENCE: 5
302 Met Ile Glu Phe Val Tyr Pro His Thr Gln Leu Val Ala Gly Val Asp
303 1               5               10              15
305 Glu Val Gly Arg Gly Pro Leu Val Gly Ala Val Val Thr Ala Ala Val
306             20              25              30
308 Ile Leu Asp Pro Ala Arg Pro Ile Ala Gly Leu Asn Asp Ser Lys Lys
309         35              40              45
311 Leu Ser Glu Lys Arg Arg Leu Ala Leu Tyr Glu Glu Ile Lys Glu Lys
312         50              55              60
314 Ala Leu Ser Trp Ser Leu Gly Arg Ala Glu Pro His Glu Ile Asp Glu
315 65              70              75              80
317 Leu Asn Ile Leu His Ala Thr Met Leu Ala Met Gln Arg Ala Val Ala
318             85              90              95
320 Gly Leu His Ile Ala Pro Glu Tyr Val Leu Ile Asp Gly Asn Arg Cys
321             100             105             110
323 Pro Lys Leu Pro Met Pro Ala Met Ala Val Val Lys Gly Asp Ser Arg
324         115             120             125
326 Val Pro Glu Ile Ser Ala Ala Ser Ile Leu Ala Lys Val Thr Arg Asp
327         130             135             140
```

RAW SEQUENCE LISTING   DATE: 05/17/2001
PATENT APPLICATION: US/09/781,712A   TIME: 10:13:22

Input Set : A:\es.txt
Output Set: N:\CRF3\05172001\I781712A.raw

```
329 Ala Glu Met Ala Ala Leu Asp Ile Val Phe Pro Gln Tyr Gly Phe Ala
330 145             150             155             160
332 Gln His Lys Gly Tyr Pro Thr Ala Phe His Leu Glu Lys Leu Ala Glu
333             165             170             175
335 His Gly Ala Thr Glu His His Arg Arg Ser Phe Gly Pro Val Lys Arg
336             180             185             190
338 Ala Leu Gly Leu Ala Ser
339         195
341 <210> SEQ ID NO: 6
343 <211> LENGTH: 286
345 <212> TYPE: PRT
347 <213> ORGANISM: Homo sapiens
351 <300> PUBLICATION INFORMATION:
353 <302> TITLE: Human Type 2 RNase H
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W--> 355 ~~<309> DATABASE ENTRY DATE:~~   → Do not enter <309> if you do
W--> 357 <310> PATENT DOC NO: US/09/203,726   not have a <308> Database Accession
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359 <311> PATENT FILING DATE: 1998-12-02                    number
361 <312> PUBLICATION DATE: 1999-12-14
365 <400> SEQUENCE: 6
367 Met Ser Trp Leu Leu Phe Leu Ala His Arg Val Ala Leu Ala Ala Leu
368 1           5               10              15
370 Pro Cys Arg Arg Gly Ser Arg Gly Phe Gly Met Phe Tyr Ala Val Arg
371             20              25              30
373 Arg Gly Arg Lys Thr Gly Val Phe Leu Thr Trp Asn Glu Cys Arg Ala
374             35              40              45
376 Gln Val Asp Arg Phe Pro Ala Ala Arg Phe Lys Lys Phe Ala Thr Glu
377     50              55              60
379 Asp Glu Ala Trp Ala Phe Val Arg Lys Ser Ala Ser Pro Glu Val Ser
380 65              70              75              80
382 Glu Gly His Glu Asn Gln His Gly Gln Glu Ser Glu Ala Lys Pro Gly
383             85              90              95
385 Lys Arg Leu Arg Glu Pro Leu Asp Gly Asp Gly His Glu Ser Ala Gln
386             100             105             110
388 Pro Tyr Ala Lys His Met Lys Pro Ser Val Glu Pro Ala Pro Pro Val
389     115             120             125
391 Ser Arg Asp Thr Phe Ser Tyr Met Gly Asp Phe Val Val Val Tyr Thr
392     130             135             140
394 Asp Gly Cys Cys Ser Ser Asn Gly Arg Arg Lys Pro Arg Ala Gly Ile
395 145             150             155             160
397 Gly Val Tyr Trp Gly Pro Gly His Pro Leu Asn Val Gly Ile Arg Leu
398             165             170             175
400 Pro Gly Arg Gln Thr Asn Gln Arg Ala Glu Ile His Ala Ala Cys Lys
401             180             185             190
403 Ala Ile Glu Gln Ala Lys Thr Gln Asn Ile Asn Lys Leu Val Leu Tyr
404             195             200             205
406 Thr Asp Ser Met Phe Thr Ile Asn Gly Ile Thr Asn Trp Val Gln Gly
407     210             215             220
409 Trp Lys Lys Asn Gly Trp Lys Thr Ser Ala Gly Lys Glu Val Ile Asn
410 225             230             235             240
```

<210> 13   Seq. #13

<211> 20

<212> DNA

<213> (Artificial)

<220>

<223> Sense primer

<400> 13
agcaggcgcc gcttcgaggc   20

<210> 14   Seq #14

<211> 26

<212> DNA

<213> (Artificial)

<220>

<223> Sense primer

<400> 14
cccgctcctg cagtattagt tcttgc   26

<210> 15   Seq # 15

<211> 25

<212> DNA

<213> (Artificial)

<220>

<223> Sense primer

<400> 15
ttgcagctgg tggtggcggc tgagg   25

Circled <213> responses are incomplete as per section 1.823b of the new sequence rules. See #11 on the Error Summary Sheet.

Note: This error occurs throughout the sequence listing. please review and correct.

VERIFICATION SUMMARY　　　　　　　　DATE: 05/17/2001
PATENT APPLICATION:　 US/09/781,712A　　　TIME: 10:13:23

Input Set : **A:\es.txt**
Output Set: **N:\CRF3\05172001\I781712A.raw**

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L:355  M:286 W: Invalid Database Entry: Valid Formats YYYY-MM-DD or Mon-YYYY, SEQ ID:6
L:357  M:284 W: Blank Line not Allowed, <310> field identifier
L:908  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:926  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:945  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:963  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:981  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:999  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:1017 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:1035 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:1053 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:1071 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:1089 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:1107 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:1126 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:1144 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:1162 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:1181 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:1199 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:1217 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:1235 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:1253 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:1271 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:1289 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:1307 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35
L:1325 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:36
L:1343 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:37
L:1361 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38
L:1379 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39
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